

Appendix B

```
***** [align] *****  
options = -align -type=protein -matrix=blosum -gapdist=8 -maxdiv=40 -outorder=aligned -gapopen=10 -gapext=0.2 -pwmatrix=blosum -pwgapopen=10 -pwgapext=0.1  
CLUSTAL W (1.83) Multiple Sequence Alignments
```

```
Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: E1-A0209P-2      498 aa
Sequence 2: E1-A0209P-8      459 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 34
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:                                Delayed
Sequence:2      Score:2988
Alignment Score 779
```

query.aln CLUSTAL W (1.83) multiple sequence alignment

query.dnd
(E1-A0209P-2:0.32789, E1-A0209P-8:0.32789);

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